

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/590,705
Source: IFW0
Date Processed by STIC: 09/05/2006

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 09/05/2006

PATENT APPLICATION: US/10/590,705

TIME: 15:10:31

Input Set : A:\5.1301 Sequence Listing.txt

Output Set: N:\CRF4\09052006\J590705.raw

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3 <110> APPLICANT: KYOWA HAKKO KOGYO CO., LTD
5 <120> TITLE OF INVENTION: Method for producing amino acid
7 <130> FILE REFERENCE: 1657
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/590,705
C--> 9 <141> CURRENT FILING DATE: 2006-08-25
9 <160> NUMBER OF SEQ ID NOS: 16
10 <170> SOFTWARE: PatentIn Ver. 3.1
12 <210> SEQ ID NO: 1
13 <211> LENGTH: 30
14 <212> TYPE: DNA
15 <213> ORGANISM: Artificial
17 <220> FEATURE:
18 <223> OTHER INFORMATION: Synthetic DNA
20 <400> SEQUENCE: 1
21 ctgcttgccc tgcaggtgca ccagcaaacg 30
23 <210> SEQ ID NO: 2
24 <211> LENGTH: 30
25 <212> TYPE: DNA
26 <213> ORGANISM: Artificial
28 <220> FEATURE:
29 <223> OTHER INFORMATION: Synthetic DNA
31 <400> SEQUENCE: 2
32 cgagctgctg gacaaccagg aattcagcgg 30
34 <210> SEQ ID NO: 3
35 <211> LENGTH: 1404
36 <212> TYPE: DNA
37 <213> ORGANISM: Corynebacterium glutamicum ATCC13032
39 <220> FEATURE:
40 <221> NAME/KEY: CDS
W--> 41 <222> LOCATION:
43 <400> SEQUENCE: 3
44 atg tca gtt aac cca acc cgc ccc gaa ggc ggc cgt cac cac gtc gtc 48
45 Met Ser Val Asn Pro Thr Arg Pro Glu Gly Gly Arg His His Val Val
46 1 5 10 15
48 gtc atc ggt tct ggt ttt ggt ggc ctt ttt gct gcc aag aac ctg gcc 96
49 Val Ile Gly Ser Gly Phe Gly Gly Leu Phe Ala Ala Lys Asn Leu Ala
50 20 25 30
52 aag gca gac gtc gat gtc act ctg att gac cgc acc aac cac cac ctc 144
53 Lys Ala Asp Val Asp Val Thr Leu Ile Asp Arg Thr Asn His His Leu
54 35 40 45
56 ttc cag cca ctg ctg tac caa gtg gca acc ggt atc ctc tcc tcc ggt 192
57 Phe Gln Pro Leu Leu Tyr Gln Val Ala Thr Gly Ile Leu Ser Ser Gly
58 50 55 60

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60	gaa atc gca cct tcc act cga cag atc ctg ggc tcc cag gaa aac gtc	240
61	Glu Ile Ala Pro Ser Thr Arg Gln Ile Leu Gly Ser Gln Glu Asn Val	
62	65 70 75 80	
64	aac gtc atc aag ggc gaa gtc acc gac atc aac gtc gag tcc cag act	288
65	Asn Val Ile Lys Gly Glu Val Thr Asp Ile Asn Val Glu Ser Gln Thr	
66	85 90 95	
68	gtg acc gcc tcc ctg ggc gag ttc acc cgc gtt ttt gag tac gat tcc	336
69	Val Thr Ala Ser Leu Gly Glu Phe Thr Arg Val Phe Glu Tyr Asp Ser	
70	100 105 110	
72	ttg gtc gtt ggt gct ggc gca ggt cag tcc tac ttc ggc aat gat cac	384
73	Leu Val Val Gly Ala Gly Ala Gly Gln Ser Tyr Phe Gly Asn Asp His	
74	115 120 125	
76	ttc gct gag ttc gca cct ggc atg aag tcc atc gac gat gca ctg gag	432
77	Phe Ala Glu Phe Ala Pro Gly Met Lys Ser Ile Asp Asp Ala Leu Glu	
78	130 135 140	
80	att cgt gca cgc atc atc ggt gct ttc gag cgc gct gag atc tgc gag	480
81	Ile Arg Ala Arg Ile Ile Gly Ala Phe Glu Arg Ala Glu Ile Cys Glu	
82	145 150 155 160	
84	gat cca gct gag cgc gaa cgc ctg ctc acc ttc gtc gtt gtt ggc gct	528
85	Asp Pro Ala Glu Arg Glu Arg Leu Leu Thr Phe Val Val Val Gly Ala	
86	165 170 175	
88	ggc cca acc ggt gtt gag ctt gct ggc cag ttg gct gag atg gct cac	576
89	Gly Pro Thr Gly Val Glu Leu Ala Gly Gln Leu Ala Glu Met Ala His	
90	180 185 190	
92	cgc acc ctt gct ggt gag tac aag aac ttc aac acc aac tcc gca aag	624
93	Arg Thr Leu Ala Gly Glu Tyr Lys Asn Phe Asn Thr Asn Ser Ala Lys	
94	195 200 205	
96	atc atc ctg ctt gat ggt gct cca cag gtt ctt cct cca ttc ggt aag	672
97	Ile Ile Leu Leu Asp Gly Ala Pro Gln Val Leu Pro Pro Phe Gly Lys	
98	210 215 220	
100	cgc cta ggc cgc aac gca cag cgc acc ctg gaa aag atg ggt gtc aac	720
101	Arg Leu Gly Arg Asn Ala Gln Arg Thr Leu Glu Lys Met Gly Val Asn	
102	225 230 235 240	
104	gtt cgc ctg aac gct atg gtc acc aac gtt gac gct acc tcg gtc acc	768
105	Val Arg Leu Asn Ala Met Val Thr Asn Val Asp Ala Thr Ser Val Thr	
106	245 250 255	
108	tac aag acc aag gac ggc gaa gag cac acc atc gaa tct ttc tgc aag	816
109	Tyr Lys Thr Lys Asp Gly Glu Glu His Thr Ile Glu Ser Phe Cys Lys	
110	260 265 270	
112	att tgg tcc gct ggt gtt gcg gca tcc cca ctg ggc aag ctc gtc gca	864
113	Ile Trp Ser Ala Gly Val Ala Ala Ser Pro Leu Gly Lys Leu Val Ala	
114	275 280 285	
116	gag cag acc ggt gtt gag acc gac cgc gca ggc cgc gtc atg gtt aac	912
117	Glu Gln Thr Gly Val Glu Thr Asp Arg Ala Gly Arg Val Met Val Asn	
118	290 295 300	
120	gat gac ctg tct gtt ggc gat cag aag aac gtc ttc gtt gtt ggc gac	960
121	Asp Asp Leu Ser Val Gly Asp Gln Lys Asn Val Phe Val Val Gly Asp	
122	305 310 315 320	
124	atg atg aac tac aac aac ctc cct ggt gtt gct cag gta gca atc cag	1008

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125 Met Met Asn Tyr Asn Asn Leu Pro Gly Val Ala Gln Val Ala Ile Gln
126          325          330          335
128 agt ggt gag tac gtt gct gag cag atc gaa gct gag gtt gaa ggc cgc 1056
129 Ser Gly Glu Tyr Val Ala Glu Gln Ile Glu Ala Glu Val Glu Gly Arg
130          340          345          350
132 tcc aac acc gag cgc gaa gct ttc gat tac ttc gac aag ggc tcc atg 1104
133 Ser Asn Thr Glu Arg Glu Ala Phe Asp Tyr Phe Asp Lys Gly Ser Met
134          355          360          365
136 gct acc att tcc cgc ttc tcc gca gtg gtg aag atg ggc aag gtt gag 1152
137 Ala Thr Ile Ser Arg Phe Ser Ala Val Val Lys Met Gly Lys Val Glu
138          370          375          380
140 gtc acc ggc ttc atc ggt tgg gtt ctg tgg ttg gct gtt cac atc atg 1200
141 Val Thr Gly Phe Ile Gly Trp Val Leu Trp Leu Ala Val His Ile Met
142 385          390          395          400
144 ttc ctg gtt ggc ttc cgc aac cgt ttc gtc tcc gca atc agc tgg ggc 1248
145 Phe Leu Val Gly Phe Arg Asn Arg Phe Val Ser Ala Ile Ser Trp Gly
146          405          410          415
148 ctg aac gca ctg tcc cgc aag cgt tgg aac ctg gca acc acc cgc cag 1296
149 Leu Asn Ala Leu Ser Arg Lys Arg Trp Asn Leu Ala Thr Thr Arg Gln
150          420          425          430
152 cag ctc cac tca cgc acc acg ctg tcc aag ttc gct cac gag ctt gag 1344
153 Gln Leu His Ser Arg Thr Thr Leu Ser Lys Phe Ala His Glu Leu Glu
154          435          440          445
156 gaa gca tct tct gat ctt cca atc gag ctg cgc gac aac cag cgt ttc 1392
157 Glu Ala Ser Ser Asp Leu Pro Ile Glu Leu Arg Asp Asn Gln Arg Phe
158          450          455          460
160 agc gga aag taa 1404
161 Ser Gly Lys
162 465
164 <210> SEQ ID NO: 4
165 <211> LENGTH: 467
166 <212> TYPE: PRT
167 <213> ORGANISM: Corynebacterium glutamicum ATCC13032
169 <400> SEQUENCE: 4
170 Met Ser Val Asn Pro Thr Arg Pro Glu Gly Gly Arg His His Val Val
171 1 5 10 15
173 Val Ile Gly Ser Gly Phe Gly Gly Leu Phe Ala Ala Lys Asn Leu Ala
174 20 25 30
176 Lys Ala Asp Val Asp Val Thr Leu Ile Asp Arg Thr Asn His His Leu
177 35 40 45
179 Phe Gln Pro Leu Leu Tyr Gln Val Ala Thr Gly Ile Leu Ser Ser Gly
180 50 55 60
183 Glu Ile Ala Pro Ser Thr Arg Gln Ile Leu Gly Ser Gln Glu Asn Val
184 65 70 75 80
186 Asn Val Ile Lys Gly Glu Val Thr Asp Ile Asn Val Glu Ser Gln Thr
187 85 90 95
189 Val Thr Ala Ser Leu Gly Glu Phe Thr Arg Val Phe Glu Tyr Asp Ser
190 100 105 110
192 Leu Val Val Gly Ala Gly Ala Gly Gln Ser Tyr Phe Gly Asn Asp His

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193          115          120          125
195 Phe Ala Glu Phe Ala Pro Gly Met Lys Ser Ile Asp Asp Ala Leu Glu
196          130          135          140
198 Ile Arg Ala Arg Ile Ile Gly Ala Phe Glu Arg Ala Glu Ile Cys Glu
199 145          150          155          160
201 Asp Pro Ala Glu Arg Glu Arg Leu Leu Thr Phe Val Val Val Gly Ala
202          165          170          175
204 Gly Pro Thr Gly Val Glu Leu Ala Gly Gln Leu Ala Glu Met Ala His
205          180          185          190
207 Arg Thr Leu Ala Gly Glu Tyr Lys Asn Phe Asn Thr Asn Ser Ala Lys
208          195          200          205
210 Ile Ile Leu Leu Asp Gly Ala Pro Gln Val Leu Pro Pro Phe Gly Lys
211          210          215          220
213 Arg Leu Gly Arg Asn Ala Gln Arg Thr Leu Glu Lys Met Gly Val Asn
214 225          230          235          240
216 Val Arg Leu Asn Ala Met Val Thr Asn Val Asp Ala Thr Ser Val Thr
217          245          250          255
219 Tyr Lys Thr Lys Asp Gly Glu Glu His Thr Ile Glu Ser Phe Cys Lys
220          260          265          270
222 Ile Trp Ser Ala Gly Val Ala Ala Ser Pro Leu Gly Lys Leu Val Ala
223          275          280          285
225 Glu Gln Thr Gly Val Glu Thr Asp Arg Ala Gly Arg Val Met Val Asn
226          290          295          300
228 Asp Asp Leu Ser Val Gly Asp Gln Lys Asn Val Phe Val Val Gly Asp
229 305          310          315          320
231 Met Met Asn Tyr Asn Asn Leu Pro Gly Val Ala Gln Val Ala Ile Gln
232          325          330          335
234 Ser Gly Glu Tyr Val Ala Glu Gln Ile Glu Ala Glu Val Glu Gly Arg
235          340          345          350
237 Ser Asn Thr Glu Arg Glu Ala Phe Asp Tyr Phe Asp Lys Gly Ser Met
238          355          360          365
240 Ala Thr Ile Ser Arg Phe Ser Ala Val Val Lys Met Gly Lys Val Glu
241          370          375          380
243 Val Thr Gly Phe Ile Gly Trp Val Leu Trp Leu Ala Val His Ile Met
244 385          390          395          400
246 Phe Leu Val Gly Phe Arg Asn Arg Phe Val Ser Ala Ile Ser Trp Gly
247          405          410          415
249 Leu Asn Ala Leu Ser Arg Lys Arg Trp Asn Leu Ala Thr Thr Arg Gln
250          420          425          430
252 Gln Leu His Ser Arg Thr Thr Leu Ser Lys Phe Ala His Glu Leu Glu
253          435          440          445
255 Glu Ala Ser Ser Asp Leu Pro Ile Glu Leu Arg Asp Asn Gln Arg Phe
256          450          455          460
258 Ser Gly Lys
259 465
261 <210> SEQ ID NO: 5
263 <211> LENGTH: 1362
264 <212> TYPE: DNA
265 <213> ORGANISM: Corynebacterium diphtheriae

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267 <220> FEATURE:
268 <221> NAME/KEY: CDS
W--> 269 <222> LOCATION:
271 <400> SEQUENCE: 5
272 atg act aac acc cca ttt cgc cca gaa ggt gga cgc cac cac gtt gta 48
273 Met Thr Asn Thr Pro Phe Arg Pro Glu Gly Gly Arg His His Val Val
274 1 5 10 15
276 gtt att ggc tcc ggc ttc ggt gga cta ttc gca gtt caa aac ctc aaa 96
277 Val Ile Gly Ser Gly Phe Gly Gly Leu Phe Ala Val Gln Asn Leu Lys
278 20 25 30
280 gat gca gat gtc gat atc acc ctc atc gac cgg aca aac cac cac ctt 144
281 Asp Ala Asp Val Asp Ile Thr Leu Ile Asp Arg Thr Asn His His Leu
282 35 40 45
284 ttc cag ccg ttg ctt tac caa gta gca acc ggt atc ttg tcg tct ggt 192
285 Phe Gln Pro Leu Leu Tyr Gln Val Ala Thr Gly Ile Leu Ser Ser Gly
286 50 55 60
288 gaa atc gca cca caa acg cgt caa gtt ctt gca cag caa aat aat gtg 240
289 Glu Ile Ala Pro Gln Thr Arg Gln Val Leu Ala Gln Gln Asn Asn Val
290 65 70 75 80
292 cac gtt ctt aag gct gaa gtc acc gac att gac acc gaa tcg aag acg 288
293 His Val Leu Lys Ala Glu Val Thr Asp Ile Asp Thr Glu Ser Lys Thr
294 85 90 95
296 gtc gtc gca gac ttg gat gat tat tct aaa aca att gaa tac gat tcc 336
297 Val Val Ala Asp Leu Asp Asp Tyr Ser Lys Thr Ile Glu Tyr Asp Ser
298 100 105 110
300 ctg atc gtc gcc gct ggt gca ggt cag tct tac ttc gga aat gat cac 384
301 Leu Ile Val Ala Ala Gly Ala Gly Gln Ser Tyr Phe Gly Asn Asp His
302 115 120 125
304 ttc gcg gaa ttc gcg ccg ggt atg aaa aca atc gat gat gca ctc gaa 432
305 Phe Ala Glu Phe Ala Pro Gly Met Lys Thr Ile Asp Asp Ala Leu Glu
306 130 135 140
308 ctg cgt gcg cgc atc atc ggc gct ttc gaa cgc gca gaa atg tgc gaa 480
309 Leu Arg Ala Arg Ile Ile Gly Ala Phe Glu Arg Ala Glu Met Cys Glu
310 145 150 155 160
312 gat ccc aaa gaa cgt gaa cgc ctc ttg act ttt gtt atc gtt ggc gca 528
313 Asp Pro Lys Glu Arg Glu Arg Leu Leu Thr Phe Val Ile Val Gly Ala
314 165 170 175
317 gga cca aca ggc gta gaa ctt gca ggt cag ctg gcc gaa atg gca cac 576
318 Gly Pro Thr Gly Val Glu Leu Ala Gly Gln Leu Ala Glu Met Ala His
319 180 185 190
321 cgc acg ttg tct gga gag tac acg cag ttc acg cct tcc aac gcg aag 624
322 Arg Thr Leu Ser Gly Glu Tyr Thr Gln Phe Thr Pro Ser Asn Ala Lys
323 195 200 205
325 atc atc ctg ctt gac ggc gct cct cag gtg ctt cca ccg ttc ggc aag 672
326 Ile Ile Leu Leu Asp Gly Ala Pro Gln Val Leu Pro Pro Phe Gly Lys
327 210 215 220
329 cgt ttg ggt cgt act gca cag cgt gaa tta gaa aag att ggt gta acg 720
330 Arg Leu Gly Arg Thr Ala Gln Arg Glu Leu Glu Lys Ile Gly Val Thr
331 225 230 235 240

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RAW SEQUENCE LISTING ERROR SUMMARY
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2

VERIFICATION SUMMARY

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Input Set : A:\5.1301 Sequence Listing.txt

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:41 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:3, CDS LOCATION:
L:269 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:5, CDS LOCATION:
L:490 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:7, CDS LOCATION:
L:701 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:9, CDS LOCATION:
L:906 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:11, CDS LOCATION:
L:1113 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:13, CDS LOCATION:
L:1326 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:15, CDS LOCATION: